

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2005, 15:12:44 ; Search time 175 Seconds

(without alignments)
471.113 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 161
Sequence: 1 AGSRKANIGGRRRRRTALAG.....ANNVYKQYEDMVVEAGCCR 161

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 14555

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_tramb:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	461	1	GDF7_MOUSE
2	97	60.2	294	2	Q9BDW9
3	97	60.2	447	1	GDF7_CERAE
4	69	42.9	450	1	GDF7_HUMAN
5	69	42.9	453	2	Q75RY1
6	67	41.6	67	2	O02784
7	50	31.1	67	2	Q8K4X3
8	44	27.3	126	2	O93573
9	44	27.3	79	2	Q9DGM4
10	31	19.3	79	2	Q91700
11	29	18.0	67	2	Q8K4X4
12	29	18.0	125	1	GDF6_MOUSE
13	29	18.0	201	2	G6P158
14	29	18.0	436	1	GDF6_BOVIN
15	29	18.0	452	2	Q6HA10
16	29	18.0	454	2	Q70UT4
17	29	18.0	455	2	Q6KFI0
18	25	15.5	399	2	Q9W753
19	23	14.3	261	2	Q9W6C0
20	22	13.7	165	2	Q95UX1
21	22	13.7	166	2	Q95UX0
22	22	13.7	207	2	Q43522
23	22	13.7	336	2	Q7Q8W9
24	21	13.0	239	2	Q95UW7
25	21	13.0	267	2	Q69T79
26	21	13.0	271	2	Q69T79
27	21	13.0	271	2	Q49216
28	21	13.0	272	2	Q49228
29	21	13.0	272	2	Q7F3M4
30	21	13.0	321	2	Q69XV3
31	21	13.0	541	2	Q87BZ7

32	21	13.0	673	2	Q653C5
33	21	13.0	1504	2	Q7PSM9
34	21	13.0	1868	2	Q9WMP3
35	20	12.4	61	2	Q8RJA2
36	20	12.4	93	2	Q6Y222
37	20	12.4	106	2	Q9GP80
38	20	12.4	118	2	Q9VY86
39	20	12.4	155	2	Q9GND8
40	20	12.4	155	2	Q9GP74
41	20	12.4	156	2	Q9GNB7
42	20	12.4	156	2	Q9GP73
43	20	12.4	157	2	Q9GP77
44	20	12.4	159	2	Q95UW1
45	20	12.4	159	2	Q95UW5

ALIGNMENTS

RESULT 1
GDF7_MOUSE STANDARD; PRT; 461 AA.
ID GDF7_MOUSE
AC P43029; Q7TNX4; Q99MY1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=Gdf7; Synonyms=Gdf-7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=BALB/c; TISSUE=Testis;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-441 FROM N.A. (ISOFORM 1).
RC STRAIN=TT2;
RA Watabe A., Fujita H., Hayaishi M., Yamamoto T.;
RL Nature 368:639-643 (1994).
DE "Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex."
RN [3]
RP SEQUENCE OF 311-461 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
DE Storm B.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingstley D.M., Lee S.-U.;
RT "Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily."
RL Nature 368:639-643 (1994).
DE -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
Name=2;
Isoid=P43029-1; Sequence=Displayed;
Isoid=P43029-2; Sequence=VSP 010764;
-1- SIMILARITY: Belongs to the TGF-beta family.

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DR EMBL; AF525752; AAP97721.1; -
DR EMBL; AF254571; AKK30843.1; -

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DR EMBL; AF254570; AAK30843.1; JOINED.
DR EMBL; U08339; AAA18780.1; -.
DR PIR; S43296; S43296.
DR HSSP; P12643; 3BMP.
DR MGD; MG1:95890; Gdf7.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR002400; GF_cysknob.
DR InterPro; IPR002405; InHbIn_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Alternative splicing; CytoKine; Glycoprotein; Growth factor; Signal.
KW SIGNAL
FT SIGNAL 1 19 potential.
FT PROPEP 20 315 potential.
FT CHAIN 316 461 Growth/differentiation factor 7.
FT DISUFID 360 426 By similarity.
FT DISUFID 389 458 By similarity.
FT DISUFID 393 460 By similarity.
FT DISUFID 425 425 Interchain (By similarity).
FT DOMAIN 311 315 Poly-Gly.
FT DOMAIN 326 351 Poly-Gly.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT VARSPIC 123 130 Missing (in isoform 2).
SQ SEQUENCE 461 AA; 47890 MW; 92C2511C86DEB478 CRC64;

Query Match 100.0%; Score 161; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 1,1e-140;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGSRKANLGGRRRRRTALAGTRGAGSGGGGGGGGGGGGGGGGGAGRGHGRGRSRC 60
DB 301 AGSRKANLGGRRRRRTALAGTRGAGSGGGGGGGGGGGGGGGGGAGRGHGRGRSRC 360

QY 61 SRSLHVDPELGDWDIIIPLYEAHCHGVCDFPRLSHLEPTNNAIIQTLLNSMAPDA 120
DB 361 SRSLHVDPELGDWDIIIPLYEAHCHGVCDFPRLSHLEPTNNAIIQTLLNSMAPDA 420

QY 121 APASCCVPARLSPISILYIDANNVVKQYEDMVVEACGR 161
DB 421 APASCCVPARLSPISILYIDANNVVKQYEDMVVEACGR 461

RESULT 2
Q9BDM9 PRELIMINARY; PRT; 294 AA.
ID Q9BDM9;
AC Q9BDM9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Crenista; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
CC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Cerebral cortex motor area;
RA MEDLINE=21136583; PubMed=11238730;
RA Metakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001)
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.
DR GO; GO:0008083; F:growth factor activity; IEA.

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DR InterPro; IPR002400; GF_cysknob.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
KM NON TER 1 1
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27AF39F CRC64;

Query Match 60.2%; Score 97; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1,7e-81;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LHVDFKELGDWDIIIPLYEAHCHGVCDFPRLSHLEPTNNAIIQTLLNSMAPDAAPS 124
DB 198 LHVDFKELGDWDIIIPLYEAHCHGVCDFPRLSHLEPTNNAIIQTLLNSMAPDAAPS 257

QY 125 CCVPARLSPISILYIDANNVVKQYEDMVVEACGR 161
DB 258 CCVPARLSPISILYIDANNVVKQYEDMVVEACGR 294

RESULT 3
GDF7_CERAE
ID GDF7_CERAE STANDARD; PRT; 447 AA.
AC Q9BDM9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=GDF7;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9534;
CC [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RA MEDLINE=21136583; PubMed=11238730;
RA Metakabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- FUNCTION: May play an active role in the motor area of the primate
CC neocortex.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in the primary aera of brain
CC neocortex.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
DR EMBL; AF254569; AAK30842.1; -.
DR EMBL; AF254568; AAK30842.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW CytoKine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 potential.
FT PROPEP 20 318 potential.

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FT CHAIN 319 447 Growth/differentiation factor 7.
FT DISUPID 346 412 By similarity.
FT DISUPID 375 444 By similarity.
FT DISUPID 379 446 By similarity.
FT DISUPID 411 411 Interchain (By similarity).
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 447 AA; 46866 MW; DF46D591925A8391 CRC64;

Query Match 60.2%; Score 97; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LHVDFKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTTHAIITQLNSMAPDAPAS 124
DB 351 LHVDFKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTTHAIITQLNSMAPDAPAS 410

QY 125 CCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
DB 411 CCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 447

RESULT 4
GPD7_HUMAN STANDARD; PRT; 450 AA.
ID GPD7_HUMAN
AC Q7Z4P5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=GDF7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May play an active role in the motor area of the primate
CC neocortex (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
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CC -----
CC EMBL; AF522369; AAP97720.1; -.
CC Genew; HGNC:4222; GDF7.
CC MIM; 604651; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 19 Potential.
FT PROPEP 20 321 Potential.
FT CHAIN 322 450 Growth/differentiation factor 7.
FT DISUPID 349 415 By similarity.
FT DISUPID 378 447 By similarity.
FT DISUPID 382 449 By similarity.
FT DISUPID 414 414 Interchain (By similarity).
FT CARBOHYD 83 83 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 450 AA; 46966 MW; CDB4C617685D37BD CRC64;

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Query Match 42.9%; Score 69; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.2e-55;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDEPLRSHLEPTTHAIITQLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 152
DB 382 CDEPLRSHLEPTTHAIITQLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 444

QY 153 MVVEACGCR 161
DB 442 MVVEACGCR 450

RESULT 5
Q75RY1 PRELIMINARY; PRT; 453 AA.
ID Q75RY1
AC Q75RY1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Growth/differentiation factor 7.
GN Name=gdf7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Suzuki M., Shimokawa H., Kasugai S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB158468; BAD07014.1; -.
DR HSP; P01137; IRLA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
SQ SEQUENCE 453 AA; 47121 MW; 9FD8CB759C63DPID CRC64;

Query Match 42.9%; Score 69; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e-55;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDEPLRSHLEPTTHAIITQLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 152
DB 385 CDEPLRSHLEPTTHAIITQLNSMAPDAPASCCVPARLSPISILYIDANNVVKQYED 444

QY 153 MVVEACGCR 161
DB 445 MVVEACGCR 453

RESULT 6
Q02784 PRELIMINARY; PRT; 67 AA.
ID Q02784
AC Q02784;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth/differentiation factor-7 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
ON NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=98183403; PubMed=9514880; DOI=10.1006/bbrc.1998.8213;
RA Morome Y., Goseki-Sone M., Ishikawa I., Oida S.;
RT "Gene expression of growth and differentiation factors-5, -6, and -7
in developing bovine tooth at the root forming stage.";
RL Biochem. Biophys. Res. Commun. 244:85-90(1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB004302; BAA20364.1; -.
DR HSSP; P12643; 1ES7.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
KM Growth factor.
FT NON_TER 1 1
SQ SEQUENCE 67 AA; 7286 MW; 37B5EA34CDA8D9D9 CRC64;

Query Match 41.6%; Score 67; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.2e-54;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 PLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPARLSPISILYID 140
DB 1 PLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPARLSPISILYID 60
QY 141 AANNVYV 147
DB 61 AANNVYV 67

RESULT 7
08K4X3 PRELIMINARY; PRT; 67 AA.
AC 08K4X3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth and differentiation factor-7 (Fragment).
GN Name-gdf-7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oida S., Morome Y., Nakamura T., Terahima T.;
RT "Molecular Cloning of PCR Amplified BMP-Related Genes (GDF-5, 6 and 7)
from Rat Tooth Cells Using Modified Bluescript SK+ Vector.";
RL Journal of hard tissue biology 6:16-20(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Oida S., Sema K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB087406; BAC02715.1; -.
DR HSSP; P12643; 1ES7.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
KM Growth factor.
FT NON_TER 1 1
SQ SEQUENCE 67 AA; 7292 MW; 3AD88A34CDA81579 CRC64;

Query Match 31.1%; Score 50; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 PLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130
DB 1 PLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130

DB 1 PLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 50

RESULT 8
093573 PRELIMINARY; PRT; 126 AA.
AC 093573;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative growth/differentiation factor 6/7 (fragment).
GN Name-gdf6/7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
of a discrete class of commissural interneurons in the mouse spinal
cord.";
RL Genes Dev. 12:3394-3407(1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; P08476; 1NVU.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008151; P: cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cys_knot.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR PRINTS; PR00669; INHIBIN.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
FT NON_TER 1 1
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 27.3%; Score 44; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.1e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 FKELGWDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTL 112
DB 34 FKELGWDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTL 77

RESULT 9
09DGN4 PRELIMINARY; PRT; 413 AA.
AC 09DGN4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth/differentiation factor 16 precursor protein.
GN Name-gdf16;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368184; PubMed=10906478; DOI=10.1016/S0925-4773(00)00350-6;
RA Vokes S.A., Krieg P.A.;
RT "gdf16, a novel member of the growth/differentiation factor subgroup
of the TGF-beta superfamily, is expressed in the hindbrain and

```

RT epibranchial placodes."
RL Mech. Dev. 95:279-282(2000).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF239676; AAF9597.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0040007; P: growth; IEA.
DR InterPro; IPR002400; GF_cyknok.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 413 AA; 46510 MW; 5F1BD7D97E591F6 CRC64;

Query Match 27.3%; Score 44; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 3e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 FKEIGMDWITAPLDYEAYHCEGVCDFPLRSHLEPTNHAIIOTL 112
Db 321 FKEIGMDWITAPLDYEAYHCEGVCDFPLRSHLEPTNHAIIOTL 364

RESULT 10
ID Q91700 PRELIMINARY; PRT; 79 AA.
AC Q91700;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transforming growth factor-beta.
GN Name-activin related;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ueno N., Nishimatsu S., Suzuki A., Murakami K.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; X17324; CAA3202.1; -.
DR PIR; S21473; S21473.
DR HSSP; P18075; ILXT.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR GO; GO:0008151; P: cell growth and/or maintenance; IEA.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
SQ SEQUENCE 79 AA; 9036 MW; 7D16A38C8C2A261F CRC64;

Query Match 19.3%; Score 31; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 8.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 FKEIGMDWITAPLDYEAYHCEGVCDFPLRSHLEPTNHAIIOTL 112
Db 49 FKEIGMDWITAPLDYEAYHCEGVCDFPLRSHLEPTNHAIIOTL 364

RESULT 11

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Q8K4X4
ID Q8K4X4 PRELIMINARY; PRT; 67 AA.
AC Q8K4X4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-6 (Fragment).
GN Name-gdf-6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oida S., Morimoto Y., Nakamura T., Terashima T.;
RT "Molecular Cloning of PCR Amplified BMP-Related Genes (GDF-5, 6 and 7)
RT from Rat Tooth Cells Using Modified pBluescript SK+ Vector.";
RL Journal of Hard Tissue Biology 6:16-20(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Oida S., Sena K.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AB087405; BAC02714.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001839; TGFb_N.
DR Pfam; PF00019; TGF_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
KW Growth factor.
FT NON_TER 1 1
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7378 MW; F627E22DB1AA268F CRC64;

Query Match 18.0%; Score 29; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 YEAYHCEGVCDFPLRSHLEPTNHAIIOTL 112
Db 4 YEAYHCEGVCDFPLRSHLEPTNHAIIOTL 32

RESULT 12
ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
GN Name=gdf6; Synonyms=Gdf-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; Pubmed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-U.;
RT "Limb alterations in brachypodiam mice due to mutations in a new
RT member of the TGF beta-superfamily."
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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DR EMBL; U08338; AAA18779.1; -.

DR PIR; S43295; S43295.

DR HSSP; P08476; INYU.

DR MGD; MGI:95689; gdf6.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFb.

DR Pfam; PF00019; TGF_beta; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR00669; INHIBINA.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Cytochrome; Glycoprotein; Growth factor.

FT PROPEP 1 5 Potential.

FT CHAIN 6 125 Growth/differentiation factor 6.

FT DISULFID 24 90 By similarity.

FT DISULFID 53 122 By similarity.

FT DISULFID 57 124 By similarity.

FT DISULFID 89 89 Interchain (By similarity).

SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B748DA32 CRC64;

Query Match 18.0%; Score 29; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 9e-19; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0;

QY 84 YEAYHCEGVCDFPLRSHLEPTNHAIIQTL 112
Db 48 YEAYHCEGVCDFPLRSHLEPTNHAIIQTL 76
|||||

RESULT 13
Q6P158 PRELIMINARY; PRT; 201 AA.
AC Q6P158;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC392255 protein (Fragment).
GN Name=LOC392255;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carlini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalska U., Smallus D.E., Schnerch A., Schin J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.L.
RU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; BC043222; AAA43222.1; -.

DR HSSP; P01137; 1KLA.

DR GO; GO:0008083; F: growth factor activity; IEA.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR001839; TGFb.

DR Pfam; PF00019; TGF_beta; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Growth factor.

FT NON_TER 1 1

SQ SEQUENCE 201 AA; 22441 MW; FF1ID52EE0517A CRC64;

Query Match 18.0%; Score 29; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0;

QY 84 YEAYHCEGVCDFPLRSHLEPTNHAIIQTL 112
Db 124 YEAYHCEGVCDFPLRSHLEPTNHAIIQTL 152
|||||

RESULT 14
ID GDF6_BOVIN STANDARD; PRT; 436 AA.
AC P5106;
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
DE morphogenetic protein 2) (CDMP-2) (Fragment).
GN Name=GDF6; Synonyms=CDMP2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.,
RT "Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed in
RT long bones during human embryonic development."
J. Biol. Chem. 269:28227-28234 (1994).
RL -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----

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CC -----

DR EMBL; U13661; AAA61416.1; -.

DR PIR; B55452; B55452.

DR HSSP; P08476; INYU.

DR InterPro; IPR009056; Cytochrome_c.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF_beta; 1.

Search completed: July 15, 2005, 15:22:25
Job time : 177 secs

DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Cysteine; Glycoprotein; Growth factor.
FT NON_TER 1 1
FT PROPEP <1 316 Potential.
FT CHAIN 317 436 Growth/differentiation factor 6.
FT DISULFID 335 401 By similarity.
FT DISULFID 364 433 By similarity.
FT DISULFID 368 435 By similarity.
FT DISULFID 400 400 Interchain (By similarity).
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 436 AA; 47873 MM; B0688R12ER8AE9ID CRC64;

Query Match 18.0%; Score 29; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 112
DB 359 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 387

RESULT 15

ID O6HA10 PRELIMINARY; PRT; 452 AA.
AC O6HA10;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Growth differentiation factor 16.
GN Name=gdf16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Guo J.H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537426; CAD60936.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cyknod.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
SQ SEQUENCE 452 AA; 51013 MM; DF756875E4C1B52A CRC64;

Query Match 18.0%; Score 29; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 2.6e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 112
DB 375 YEAYHCEGVCDPPLRSHLEPTNHAIIQTL 403

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OM protein - protein search, using sw model

Run on: July 15, 2005, 15:09:02 ; Search time 161 Seconds

(without alignments)
386.760 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 161

Sequence: 1 AGSRKANLGRRRRRTALAG.....ANNVVYKQYEDMVVEACGCR 161

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 6

Total number of hits satisfying chosen parameters: 20433

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	161	2	AAR65182
2	151	93.8	151	6	ABG76038
3	151	93.8	151	8	ADG14199
4	146	90.7	146	5	AAW51934
5	102	63.4	102	3	AAV92582
6	102	63.4	102	3	AAW09557
7	102	63.4	102	3	AAW02823
8	100	62.1	100	2	AAR78738
9	100	62.1	100	2	AAW26594
10	100	62.1	100	2	AAE10984
11	100	62.1	100	6	ABG73300
12	72	44.7	72	4	AAE10977
13	72	44.7	72	6	ABG73293
14	69	42.9	102	3	AAW09558
15	69	42.9	102	3	AAW02824
16	69	42.9	104	8	ADH11612
17	69	42.9	104	8	ADH05310
18	69	42.9	129	2	AAW54067
19	69	42.9	184	4	ABG29375
20	69	42.9	294	2	AAR78729
21	69	42.9	294	2	AAW26589
22	69	42.9	294	4	AAE10972
23	69	42.9	294	6	ABG73289
24	69	42.9	388	2	AAR78734
25	69	42.9	388	2	AAW26592

26	69	42.9	388	4	AAE10986	AAE10986 Human bon
27	69	42.9	388	6	ABG73302	ABG73302 Human bon
28	69	42.9	388	8	ADH11588	ADH11588 Human bon
29	69	42.9	411	2	AAR78740	AAR78740 Fusion of
30	69	42.9	411	2	AAW26597	AAW26597 BMP-2 pro
31	69	42.9	411	4	AAE10983	AAE10983 Human BMP
32	69	42.9	411	6	ABG73299	ABG73299 Human BMP
33	69	42.9	450	6	ABJ37118	ABJ37118 NOVX prot
34	69	42.9	450	6	ABP57347	ABP57347 Human sec
35	69	42.9	450	7	ADM78335	ADM78335 Human gro
36	40	24.8	430	7	ADM78336	ADM78336 Human gro
37	39	24.2	72	2	AAR78735	AAR78735 Murine ho
38	37	23.0	37	3	AAW09497	AAW09497 Murine ho
39	35	21.7	35	3	AAV92535	AAV92535 Finger 2
40	35	21.7	35	3	AAW02764	AAW02764 Mouse GDF
41	34	21.1	34	8	ADG14200	ADG14200 Mouse GDF
42	34	21.1	34	8	ADG14202	ADG14202 Mouse GDF
43	33	20.5	33	8	ADG14201	ADG14201 Mouse GDF
44	31	19.3	65	2	AAR10994	AAR10994 Xenopus B
45	29	18.0	72	2	AAR78736	AAR78736 Murine bo

ALIGNMENTS

RESULT 1	
AAE65182	
ID	AAE65182 standard; protein: 161 AA.
XX	
AC	AAE65182;
XX	
DT	25-MAR-2003 (revised)
DT	14-AUG-1995 (first entry)
XX	
DE	GDF-7 C-terminal region.
XX	
KM	GDF-7; growth differentiation factor 7; TGF-beta;
KW	transforming growth factor-beta; proliferative disorder; neural cell;
KM	diagnosis; gene therapy.
XX	
OS	Mus sp.
XX	
FH	Key
FT	Cleavage-site
FT	Location/Qualifiers
FT	11..15
FT	/note="Cleavage at this site generates a mature C-terminal fragment of 146 amino acids (mol.wt. 14,500)"
XX	
PN	W09501802-A1.
XX	
PD	19-JAN-1995.
XX	
PF	08-JUL-1994; 94W0-US007799.
XX	
PR	09-JUL-1993; 93US-00089670.
XX	
PA	(UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX	
PI	Lee S, Huynh T;
XX	
DR	WPI: 1995-066739/09.
XX	
FT	N-PSDB; AAQ82824.
XX	
PT	Pure growth differentiation factor-7 and antibodies against it - used to detect GDF-7 associated cell proliferative disorders, pref. in neural cells, in vivo or in vitro.
XX	
PS	Disclosure; Page 31-32; 60pp; English.
XX	
CC	DNA encoding the C-terminal region of a novel member of the TGF-beta superfamily, growth differentiation factor-7 (GDF-7), was obtained by PCR amplification of mouse genomic DNA using primers based on conserved sequences of known family members. GDF-7 and encoding sequences have diagnostic and therapeutic uses, including gene therapy via retrovirus-

Query Match	100.0%	Score 161	DB 2	Length 161
Best Local Similarity	100.0%	Pred. No. 7,7e-145		
Matches 161	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	AGSRKANIIGRRRRRTALAGTGAAGCGGGGGGGGGGGGGGGGGAGRGHGRGRSFC	60	
Db	1	AGSRKANIIGRRRRRTALAGTGAAGCGGGGGGGGGGGGGGGGGAGRGHGRGRSFC	60	
QY	61	SRKSLHVDPEKELGMDWMIAPLDVEAYHVEGVCDDPRLRSHLEPTNNAIIQTLLNSMAPA	120	
Db	61	SRKSLHVDPEKELGMDWMIAPLDVEAYHVEGVCDDPRLRSHLEPTNNAIIQTLLNSMAPA	120	
QY	121	APASCCVPARLSPISILYIDANNVYVKQEDMVVEACGCR	161	
Db	121	APASCCVPARLSPISILYIDANNVYVKQEDMVVEACGCR	161	
RESULT 2				
ABG76038				
ID	ABG76038	standard; protein; 151 AA.		
XX	ABG76038;			
AC				
XX				
DT	30-APR-2003	(first entry)		
XX				
DE	Human GDF-7 C-terminus.			
XX				
KM	GDF-5; growth differentiation factor 5; TGF-beta; human;			
KM	transforming growth factor beta; skeletal development; endometriosis;			
KM	cartilage differentiation; cell proliferative disease; uterine tumour;			
KM	bone dysplasia; spondyloepiphyseal dysplasia; achondroplasia;			
KM	dysplasia epiphysealis; metaphyseal dysostosis; hyperchondroplasia;			
KM	enchondromatosis; hypophosphatasia; osteopetrosis; hyperphosphatasia;			
KM	craniofacial dysplasia; osteogenesis imperfecta; transgenic;			
KM	idiopathic osteoporosis; Engelman's disease; GDF-7.			
XX				
OS	Homo sapiens.			
XX				
PN	US2002165361-A1.			
PD	07-NOV-2002.			
XX				
PP	12-JUN-2001; 2001US-00880708.			
XX				
PR	12-JAN-1993; 93US-00003144.			
PR	12-JAN-1994; 94WO-US000657.			
PR	31-MAY-1995; 95US-00455559.			
PR	01-SEP-1998; 98US-00145060.			
XX				
PA	(LEES/) LEE S.			
PA	(HUTN/) HUTNH T.			
XX				
P1	Lee S, Huynh T;			
XX				
DR	WPI, 2003-255226/25.			
XX				
PT	New antibody specifically binding to a GDF-5 polypeptide, useful for			
PT	diagnosing and treating cell proliferative disorders with aberrant GDF-5			
PT	activity, such as endometriosis, uterine tumors and those involving			
PT	skeletal tissues.			
XX				
PS	Example 2; Fig 3B; 36pp; English.			
CC	The invention relates to an antibody that specifically binds to growth			
CC	differentiation factor-5 (GDF-5, a member of the TGF-Beta (transforming			
CC	growth factor beta) superfamily of proteins) polypeptide appearing as			
CC	ABG76038. In order to determine the biological activity of GDF-5 in vivo,			
CC	transgenic mice were constructed that express GDF-5 ectopically. Analysis			
CC	of two independent transgenic mouse lines showed that these animals have			

CC	ectopic bone formation with evident muscle tissue. This showed that GDF-5
CC	was capable of inducing bone formation in vivo. The antibody is useful
CC	for the diagnosis and treatment of cell proliferative disorders
CC	associated with aberrant GDF-5 activity, such as endometriosis, uterine
CC	tumors, those involving skeletal tissues, endometriosis, cartilage
CC	differentiation, cell proliferative disease, uterine tumour, bone
CC	dysplasia, spondyloilthyseal dysplasia, achondroplasia, dysplasia
CC	epiphyseals, metaphyseal dysostosis, hyperchondroplasia,
CC	enchondromatosis, hypophosphataemia, osteopetrosis, hyphosphataemia,
CC	craniolethophysal dysplasia, osteogenesis imperfecta, idiopathic
CC	osteoporosis and Engelmann's disease. The present sequence represents a
CC	member of the TGFbeta superfamily used to determine regions of sequence
XX	similarity for design of degenerate primers for isolation of GDF-5
XX	Sequence 151 AA:
SQ	
Query Match	93.8%; Score 151; DB 6; Length 151;
Best Local Similarity	100.0%; Pred. No. 2.4e-15;
Matches 151;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	11 RRRRTTALAGTRGAQGSGGGGCGGGGGGGGGGAGRGHGRGRRCRCKSLHYDPK 70
DB	1 RRRRTTALAGTRGAQGSGGGGCGGGGGGGGGGAGRGHGRGRRCRCKSLHYDPK 60
OY	71 ELGWDDWIIAPLDYEAVHCBGVCPPLRSHEPTTHAIIITLLNSMAPDAAPASCCVPAR 130
DB	61 ELGWDDWIIAPLDYEAVHCBGVCPPLRSHEPTTHAIIITLLNSMAPDAAPASCCVPAR 120
OY	131 LSPISILYIDANNVVVKQYEDMVEACGCC 161
DB	121 LSPISILYIDANNVVVKQYEDMVEACGCC 151
RESULT 3	
ID ADG14199	ADG14199 standard; protein; 151 AA.
XX AC	ADG14199;
XX DT	26-FEB-2004 (first entry)
XX DE	Mouse full length GDF7 protein.
KW	Mouse; osteogenic protein-1; OP-1; transforming growth factor beta;
KW	TGfbeta; bone morphogenic protein; BMP5; BMP6; BMP2; BMP4; BMP8/OP2;
KW	Growth Differentiation Factor; GDF5; GDF6; GDF7; cell growth;
XX OS	Mus musculus.
XX PN	US2003185792-A1.
PD	02-OCT-2003.
PF	06-JUN-2002; 2002US-00164279.
PR	22-JAN-1996; 96US-00589552.
PR	22-JAN-1997; 97US-00786284.
PR	22-FEB-2001; 2001US-00791946.
PR	06-JUN-2001; 2001US-0296291P.
PR	05-FEB-2002; 2002US-0354820P.
PR	10-APR-2002; 2002US-0371298P.
PA	(CURI-) CURIS INC.
P1	Keck PC, Boenkonda D;
DR	WP1; 2004-031977/03.
PT	Bone morphogenic protein antagonist peptide comprises peptide sequence
XX	having specified amino acid residues including contiguous amino acids of
XX	specific amino acid sequences given in the specifications.

DR WPI; 2000-303743/26.
 XX
 XX A biologically active TGF-beta family member fusion protein competent to
 PT refold, comprising a C-terminal linked TGF-beta family protein.
 PT
 PS Disclosure; Page 160; 160pp; English.
 XX
 XX AAY2554-82 show the finger 1, heel and finger 2 domains of TGF-beta
 CC superfamily members. These sequences can be used to form novel fusion
 CC proteins. Novel proteins comprise biologically active TGF-beta family
 CC member fusion proteins competent to refold under suitable refolding
 CC conditions. The fusion proteins comprise: (1) a TGF-beta family protein C
 CC-terminal seven cysteine domain, comprising finger 1, finger 2 and heel
 CC subdomains; and (2) a heterologous leader sequence domain operatively
 CC linked to the C-terminal domain. Truncations, heterodimers and mutants of
 CC these fusion proteins and methods of purifying the heterodimers are also
 CC claimed. The TGF-beta family proteins can be used to induce the full
 CC cascade of morphogenic events which culminate in skeletal tissue
 CC formation, including cartilage and endochondral bone formation. They are
 CC useful in the binding of fibrin and fibronectin to the implanted matrix,
 CC chondroblasts, cartilage formation, vascular invasion, bone formation,
 CC remodeling, and bone marrow differentiation. The proteins have improved
 CC physical properties such as solubility and stability, improved biological
 CC activity, including altered receptor binding and improved targeting
 CC capabilities
 XX
 SQ Sequence 102 AA;
 Query Match 63.4%; Score 102; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 6.8e-99;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 CSRSKSLHVDPKELGMDWIIAPLDYEAHYHCEGVCDFPLRSHLEPTNHAIIQTLSNAPD 119
 DB 1 CSRSKSLHVDPKELGMDWIIAPLDYEAHYHCEGVCDFPLRSHLEPTNHAIIQTLSNAPD 60
 QY 120 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 61 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 102
 RESULT 6
 AAB09557
 ID AAB09557 standard; protein; 102 AA.
 AC AAB09557;
 DT 11-SEP-2000 (first entry)
 DE Murine GDF-7, SEQ ID NO:87.
 XX
 XX TGF-beta superfamily; transforming growth factor-beta;
 KM developmental regulation; finger 2 subdomain; basic region;
 KM protein refolding; stability; solubility; osteogenic protein; OP;
 KM bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KM inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
 KM connective tissue; cartilage; vulnary.
 XX
 XX Mus musculus.
 OS
 PN MO200020607-A2.
 PD 13-APR-2000.
 XX
 XX 07-OCT-1999; 99W0-US023371.
 PF
 XX 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374958.
 XX
 XX (STYC) STRYKER CORP.
 PA
 XX Oppermann H, Tai M, McCartney J;
 PI

XX
 DR WPI; 2000-303787/26.
 XX
 XX Transforming growth factor-beta superfamily member mutant induces tissue
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.
 PS Disclosure; Page 161-162; 162pp; English.
 XX
 XX The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC-terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralized skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralized skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and
 CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequence AAB09519-B09542 and
 CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily
 CC proteins referred to in the specification
 XX
 SQ Sequence 102 AA;
 Query Match 63.4%; Score 102; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 6.8e-89;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 CSRSKSLHVDPKELGMDWIIAPLDYEAHYHCEGVCDFPLRSHLEPTNHAIIQTLSNAPD 119
 DB 1 CSRSKSLHVDPKELGMDWIIAPLDYEAHYHCEGVCDFPLRSHLEPTNHAIIQTLSNAPD 60
 QY 120 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 61 AAPASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 102
 RESULT 7
 AAB02823
 ID AAB02823 standard; protein; 102 AA.
 AC AAB02823;
 DT 22-AUG-2000 (first entry)
 DE Mouse GDF-7 amino acid sequence SEQ ID NO:87.
 XX
 XX
 XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KM bone morphogenic protein; osteogenic protein; mutant; modified;
 KM finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KM osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KM tissue repair; regeneration; proliferation; differentiation.
 XX
 XX Mus musculus.
 OS
 XX
 PN MO200020591-A2.
 PI

PD 13-APR-2000.
 XX
 PF 07-OCT-1999; 99WO-US023370.
 XX
 PR 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374936.
 XX
 PA (STRYK) STRYKER CORP.
 XX
 PI Oppermann H, Tai M, McCartney J;
 DR WPI; 2000-303776/26.
 XX
 PT Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.
 XX
 PS Disclosure; Page 148; 149pp; English.
 XX
 CC The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that
 CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair
 CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
 CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
 CC and for inducing the proliferation and differentiation of uncommitted
 CC progenitor cells in a tissue-specific manner to support new tissue
 CC formation. AA029887 to AA029897 and AA02748 to AA02824 represent
 CC sequences used in the exemplification of the present invention
 CC
 SQ Sequence 102, AA;
 XX
 Query Match 63.4%; Score 102; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 6.8e-69;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 60 CSRKSLHVDPEKELGMDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPD 119
 DB 1 CSRKSLHVDPEKELGMDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPD 60
 QY 120 AAPASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
 DB 61 AAPASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 102
 RESULT 8
 AAR78738 standard; protein; 240 AA.
 XX
 AC AAR78738;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-NOV-1995 (first entry)
 XX
 DE Murine mV1 protein.
 XX
 KM Bone morphogenetic protein; mV1; tendon; ligament.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 7 /label= V,A,E,G
 FT Misc-difference 8 /label= S,P,T,A
 FT Misc-difference 15 /label= S,R
 FT

FT Misc-difference 16 /label= L,P,Q,R
 FT Misc-difference 26 /label= C,W
 FT Misc-difference 37 /label= V,A,D,G
 FT Misc-difference 103 /label= V,A,E,G
 FT Misc-difference 104 /label= Q,K,E
 XX
 PN W09516035-A2.
 XX
 PD 15-JUN-1995.
 XX
 PF 06-DEC-1994; 94WO-US014030.
 XX
 PR 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 XX
 PA (GENY) GENETICS INST. INC.
 PA (HARD) HARVARD COLLEGE.
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 DR WPI; 1995-224320/29.
 DR N-PSDB; AA096223.
 XX
 PT Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 PT compar. for inducing tendon/ligament-like tissue formation.
 XX
 PS Example; Page 68-70; 84pp; English.
 XX
 CC Oligos #6 and #7 (AA096223 & AA096219) are used as primers for the
 CC amplification of a 275 bp DNA probe, the internal 269 bp of which
 CC corresp. to nt# 607 to nt# 865 of AA096207, from the BMP-12 encoding
 CC plasmid subclone PCR1-1#2. This probe was radioactively labelled and used
 CC to screen a murine genomic library. DNA sequence analysis of one of
 CC positively hybridising recombinants named MVR3 indicates that it encodes
 CC a portion of the mouse gene corresp. to the PCR product mV1 (murine
 CC homolog of the human BMP-12 sequence AA096207. The partial DNA sequence
 CC of this subclone and corresp. AA translation are given in AA096223 &
 CC AAR78738. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 240 AA;
 XX
 Query Match 62.1%; Score 100; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 RKSILHVDPEKELGMDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 121
 DB 141 RKSILHVDPEKELGMDWIIAPLDYEAVHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 200
 QY 122 PASCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
 DB 201 PASCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 240
 RESULT 9
 AAM26594 standard; protein; 240 AA.
 XX
 AC AAM26594;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUN-1998 (first entry)
 XX
 DE Murine BMP-12 homologue fragment.
 XX
 KM BMP-12; bone morphogenetic protein; mouse; tendon; ligament;
 XX

KM wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
 KM therapy.
 XX
 OS Mus musculus.
 XX
 Key Location/Qualifiers
 FT Misc-difference 7 /label= Val, Ala, Glu, Gly
 FT /note= "encoded by GNC"
 FT Misc-difference 8 /label= Ser, Pro, Thr, Ala
 FT /note= "encoded by NCG"
 FT Misc-difference 15 /label= Ser, Arg
 FT /note= "encoded by AGN"
 FT Misc-difference 16 /label= Leu, Pro, Glu, Arg
 FT /note= "encoded by GNC"
 FT Misc-difference 26 /label= Cys, Tyr
 FT /note= "encoded by TGN"
 FT Misc-difference 37 /label= Val, Ala, Asp, Gly
 FT /note= "encoded by GNC"
 FT Misc-difference 103 /label= Val, Ala, Glu, Gly
 FT /note= "encoded by GNC"
 FT Misc-difference 104 /label= Lys, Gln
 FT /note= "encoded by NAG"
 XX
 PN US568882-A.
 PD 19-AUG-1997.
 XX
 PF 22-DEC-1994; 94US-00362670.
 XX
 PR 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Melton DA, Thomsen GH, Wozney JM, Wolfman NM, Rosen VA;
 PI Celeste AJ;
 DR WPI; 1997-424270/39.
 DR N-PSDB; AAT90396.
 XX
 PT Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52 -
 PT useful for tissue healing and repair, treatment of tendonitis, improving
 PT fixation of tendons to bone etc.
 XX
 PS Example 1; Col 65-68; 43pp; English.
 XX
 CC This polypeptide comprises a fragment of a murine homologue of human bone
 CC morphogenetic protein 12 (BMP-12) (see also AAW26589). Its amino acid
 CC sequence was deduced from DNA subclone mV1 (see AAT90396), isolated from
 CC murine genomic DNA using primers (see AAT90393-94) based on human BMP-12
 CC sequence. Human BMP-12, BMP-13 (see AAW26591) and MP52 (see AAW26590)
 CC polypeptides are used in a claimed method for inducing tendon and
 CC ligament formation. (updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 240 AA;
 Query Match 62.1%; Score 100; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1,1e-86; Indels 0; Gaps 0;
 Matches 100; Conservative 0; Mismatches 0;
 QY 62 RKSLLHVDPKELGMDWIIAPLDYRAYHCEGVDFPLRSLHPTNHAIIQTLLNSMADDA 121
 DB 141 RKSLLHVDPKELGMDWIIAPLDYRAYHCEGVDFPLRSLHPTNHAIIQTLLNSMADDA 200

QY 122 PASCVPARLSPISILYIDANNVYKQYEDWVEACGR 161
 DB 201 PASCVPARLSPISILYIDANNVYKQYEDWVEACGR 240
 RESULT 10
 AAE10984
 ID AAE10984 standard; protein; 240 AA.
 XX
 AC AAE10984;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Murine partial mV1 protein.
 XX
 KM Mouse; bone morphogenic protein; BMP-12; vulnery; antiinflammatory;
 KM analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KM tissue formation; wound healing; tissue repair; ligament defect;
 KM carpal tunnel syndrome; tendonitis; mV1.
 XX
 OS Mus sp.
 XX
 Key Location/Qualifiers
 FT Misc-difference 7 /label= Unknown
 FT /note= "Encoded by GNC"
 FT Misc-difference 8 /label= Unknown
 FT /note= "Encoded by NCG"
 FT Misc-difference 15 /label= Unknown
 FT /note= "Encoded by AGN"
 FT Misc-difference 16 /label= Unknown
 FT /note= "Encoded by GNC"
 FT Misc-difference 26 /label= Unknown
 FT /note= "Encoded by GNC"
 FT Misc-difference 37 /label= Unknown
 FT /note= "Encoded by GNC"
 FT Misc-difference 103 /label= Unknown
 FT /note= "Encoded by GNC"
 FT Misc-difference 104 /label= Unknown
 FT /note= "Encoded by NAG"
 XX
 PN US6284872-B1.
 PD 04-SEP-2001.
 XX
 PF 28-FEB-1997; 97US-00808324.
 XX
 PR 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 PR 22-DEC-1994; 94US-00362670.
 XX
 PA (GEMY) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 DR WPI; 2001-588978/66.
 DR N-PSDB; AAD18335.
 XX
 PT New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome
 PT and other tendon and ligament defects, comprises DNA encoding propeptide
 PT linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or
 PT MP52.

XX Example 1; Col 67-70; 42pp; English.

PS The invention relates to a chimeric DNA comprising a DNA sequence

CC encoding a propeptide from a member of the transforming growth factor

CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence

CC encoding an amino acid sequence encoding a mature polypeptide consisting

CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA

CC sequences are useful for producing proteins which induce tendon/ligament

CC like tissue formation, and for isolating and cloning further DNA

CC sequences encoding BMP-12 related proteins with similar activity. The

CC proteins are useful for the induction of tendon/ligament-like tissue

CC formation, wound healing, ligament and other tissue repair, augmenting

CC the activity of bone morphogenetic proteins, and for treating tendinitis,

CC carpal tunnel syndrome and other tendon and ligament defects. The present

CC sequence is murine partial mvl protein which is homologous to human BMP-

CC 12 or VL-1 sequences of the invention

XX

XX Sequence 240 AA:

SQ

Query Match 62.1%; Score 100; DB 4; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RKSLHVDPEKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 121

DB 141 RKSLHVDPEKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 200

QY 122 PASCCTPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161

DB 201 PASCCTPARLSPISILYIDAANNVVKQYEDMVVEACGCR 240

RESULT 11

ABG73300

ID ABG73300 standard; protein; 240 AA.

XX

XX ABG73300;

AC

XX

DT 30-APR-2003 (first entry)

DE

XX

XX Amino acid sequence for murine mvl protein.

KM Mouse: bone morphogenetic protein-12; BMP-12; BMP-12 related protein;

KM BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendinitis;

KM tendon/ligament-like tissue formation; trauma induced tendon defect;

KM tendon/ligament-like tissue healing; tendon damage; ligament damage;

KM tendon fixation; ligament fixation; congenital; ligament defect;

KM cosmetic plastic surgery; vulnerability; murine; mvl.

XX

OS Mus sp.

XX

XX

XX Key Location/Qualifiers

FT Misc-difference 7

FT /label= Val, Ala, Glu, Gly

FT /note= "Encoded by GNG"

FT Misc-difference 8

FT /label= Ser, Pro, Thr, Ala

FT /note= "Encoded by NCG"

FT Misc-difference 15

FT /label= Ser, Arg

FT /note= "Encoded by AGN"

FT Misc-difference 16

FT /label= Leu, Pro, Gln, Arg

FT /note= "Encoded by CNG"

FT Misc-difference 26

FT /label= Cys, Trp

FT /note= "Encoded by TGN"

FT Misc-difference 37

FT /label= Val, Ala, Asp, Gly

FT /note= "Encoded by GNC"

FT Misc-difference 103

FT /label= Val, Ala, Glu, Gly

FT /note= "Encoded by GNG"

FT Misc-difference 104

FT /label= Gln, Lys, Glu

FT /note= "Encoded by NAG"

XX

XX US2002160494-A1.

XX

XX 31-OCT-2002.

XX

XX 31-AUG-2001; 2001US-00945182.

XX

XX 07-DEC-1993; 93US-00164103.

XX 25-MAR-1994; 94US-00217780.

XX 02-NOV-1994; 94US-00333576.

XX 22-DEC-1994; 94US-00362670.

XX 28-FEB-1997; 97US-00808324.

XX

XX (CELEST) CELESTE A J.

XX (WOZN) WOZNEY J M.

XX (ROSE) ROSEN V A.

XX (WOLF) WOLFMAN N M.

XX (THOM) THOMSEN G H.

XX (MELT) MELTON D A.

XX

XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH,

XX Melton DA;

XX WPI; 2003-238228/23.

XX N-PSDB; ABX11157.

XX

XX New bone morphogenetic proteins (designated BMP-12) or related proteins,

XX useful for inducing tendon/ligament-like tissue formation in a patient,

XX or for tendon/ligament-like tissue healing or repair (e.g. for treating

XX tendinitis).

XX

XX Example 1; Page 37; 46pp; English.

XX

XX The present invention relates to the isolation of human bone

XX morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein

XX (designated BMP-13 or VL-1), and the polynucleotide sequences encoding

XX them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of

XX proteins. BMP-12 and VL-1 are characterized by their ability to induce

XX the formation of tendon/ligament-like tissue. The BMP-12 proteins of the

XX invention are useful for inducing tendon/ligament-like tissue formation

XX in a patient. They are particularly useful for tendon/ligament-like

XX tissue healing and tissue repair, e.g. for treating tendinitis, or other

XX tendon or ligament defects in a patient. The polynucleotide sequences

XX encoding the BMP-12 proteins are useful for inducing tendon/ligament-like

XX tissue formation in a patient, and for tendon/ligament-like tissue

XX healing and tissue repair. The BMP-12 polypeptide and polynucleotide

XX sequences may be used for preventing damage to tendon or ligament tissue,

XX to improve fixation of tendon or ligament to bone or other tissues, to

XX repair congenital or trauma induced tendon or ligament defects, and in

XX cosmetic plastic surgery for attachment or repair of tendons or

XX ligaments. The present sequence represents murine mvl protein, a

XX homologue of human BMP-12/VL-1

XX

XX

SQ Sequence 240 AA:

Query Match 62.1%; Score 100; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 RKSLHVDPEKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 121

DB 141 RKSLHVDPEKELGMDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAA 200

QY 122 PASCCTPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161

DB 201 PASCCTPARLSPISILYIDAANNVVKQYEDMVVEACGCR 240

RESULT 12

AAE10977
 ID AAE10977 standard; protein; 72 AA.
 AC AAE10977;
 DT 18-DEC-2001 (first entry)
 DE Murine clone mV1 protein.
 XX
 XX Mouse; bone morphogenic protein; BMP-12; vulnery; antiinflammatory;
 KW analgesic; gene therapy; transforming growth factor-beta; TGF-beta;
 KW tissue formation; wound healing; tissue repair; ligament defect;
 KW carpal tunnel syndrome; tendonitis; mV1.
 OS Mus sp.
 XX
 XX US6284872-B1.
 PD 04-SEP-2001.
 XX
 XX 28-FEB-1997; 97US-00808324.
 PF
 XX 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 PR 22-DEC-1994; 94US-00362670.
 XX
 PA (GEMT) GENETICS INST INC.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 XX WPI; 2001-586978/66.
 DR N-PSDB; AAD18321.
 DR
 PT New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome
 PT and other tendon and ligament defects, comprises DNA encoding propeptide
 PT linked to DNA encoding bone morphogenetic proteins (BMP-12, BMP-13 or
 PT MP52.
 PT
 XX
 XX Example 1; Col 47-48; 42pp; English.
 XX
 XX The invention relates to a chimeric DNA comprising a DNA sequence
 CC encoding a propeptide from a member of the transforming growth factor
 CC (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
 CC encoding an amino acid sequence encoding a mature polypeptide consisting
 CC of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA
 CC sequences are useful for producing proteins which induce tendon/ligament
 CC like tissue formation, and for isolating and cloning further DNA
 CC sequences encoding BMP-12 related proteins with similar activity. The
 CC proteins are useful for the induction of tendon/ligament-like tissue
 CC formation, wound healing, ligament and other tissue repair, augmenting
 CC the activity of bone morphogenetic proteins, and for treating tendonitis,
 CC carpal tunnel syndrome and other tendon and ligament defects. The present
 CC sequence is murine clone, mV1 protein which is homologous to human BMP-12
 CC or VL-1 sequences of the invention
 XX
 XX Sequence 72 AA;
 SQ
 Query Match 44.7%; Score 72; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 1.7e-60;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 77 WIIAPLDYEAHYHCEGVCDPLRSHLEPTNNAIIQTLLNSAPDAAPASCCVPARLSPISI 136
 DB 1 WIIAPLDYEAHYHCEGVCDPLRSHLEPTNNAIIQTLLNSAPDAAPASCCVPARLSPISI 60
 OY 137 LYTDAANNVYK 148
 DB 61 LYTDAANNVYK 72

RESULT 13
 ABG73293
 ID ABG73293 standard; protein; 72 AA.
 AC ABG73293;
 DT 30-APR-2003 (first entry)
 DE Homologue of human BMP-12/VL-1 encoded by DNA from murine clone mV1.
 XX
 XX Mouse; bone morphogenetic protein-12; BMP-12; BMP-12 related protein;
 KW BMP-13; VL-1; BMP/TGF-beta/Vg-1 family; tissue repair; tendonitis;
 KW tendon/ligament-like tissue formation; trauma induced; ligament defect;
 KW tendon fixation; ligament healing; tendon damage; ligament damage;
 KW tendon fixation; ligament fixation; congenital; ligament defect;
 KW cosmetic plastic surgery; vulnery; murine; mV1.
 OS Mus sp.
 XX
 XX US2002160494-A1.
 PD 31-OCT-2002.
 XX
 XX 31-AUG-2001; 2001US-00945182.
 PF
 XX 07-DEC-1993; 93US-00164103.
 PR 25-MAR-1994; 94US-00217780.
 PR 02-NOV-1994; 94US-00333576.
 PR 22-DEC-1994; 94US-00362670.
 PR 28-FEB-1997; 97US-00808324.
 XX
 XX (CELE) CELESTE A J.
 XX (WOZN) WOZNEY J M.
 XX (ROSE) ROSEN V A.
 XX (WOLF) WOLFMAN N M.
 XX (THOM) THOMSEN G H.
 XX (MELT) MELTON D A.
 XX
 PI Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH;
 PI Melton DA;
 XX
 XX WPI; 2003-238228/23.
 DR N-PSDB; ABX11145.
 DR
 PT New bone morphogenetic proteins (designated BMP-12) or related proteins,
 PT useful for inducing tendon/ligament-like tissue formation in a patient,
 PT or for tendon/ligament-like tissue healing or repair (e.g. for treating
 PT tendonitis).
 PT
 XX
 XX Example 1; Page 25-26; 46pp; English.
 XX
 XX The present invention relates to the isolation of human bone
 CC morphogenetic protein-12 (BMP-12) protein and a BMP-12 related protein
 CC (designated BMP-13 or VL-1), and the polynucleotide sequences encoding
 CC them. The novel BMPs are members of the BMP/TGF-beta/Vg-1 family of
 CC proteins. BMP-12 and VL-1 are characterised by their ability to induce
 CC the formation of tendon/ligament-like tissue. The BMP-12 proteins of the
 CC invention are useful for inducing tendon/ligament-like tissue formation
 CC in a patient. They are particularly useful for tendon/ligament-like
 CC tissue healing and tissue repair, e.g. for treating tendonitis, or other
 CC tendon or ligament defects in a patient. The polynucleotide sequences
 CC encoding the BMP-12 proteins are useful for inducing tendon/ligament-like
 CC tissue formation in a patient, and for tendon/ligament-like tissue
 CC healing and tissue repair. The BMP-12 polypeptide and polynucleotide
 CC sequences may be used for preventing damage to tendon or ligament tissue,
 CC to improve fixation of tendon or ligament to bone or other tissues, to
 CC repair congenital or trauma induced tendon or ligament defects, and in
 CC cosmetic plastic surgery for attachment or repair of tendons or
 CC ligaments. The present sequence represents a homologue of human BMP-12/VL-
 CC -1 encoded by DNA from murine clone mV1
 XX
 XX Sequence 72 AA;
 SQ

Query Match 44.7%; Score 72; DB 6; Length 72;
 Best Local Similarity 100.0%; Pred. No. 1.7e-60;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 WILPDLVYAHVCGVCDPFLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISI 136
 1 WILPDLVYAHVCGVCDPFLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISI 60

Qy 137 LYIDANNVYK 148
 61 LYIDANNVYK 72

Db 61 LYIDANNVYK 72

RESULT 14
 AAB09558
 ID AAB09558 standard; protein, 102 AA.

AC AAB09558;
 XX
 XX 11-SEP-2000 (first entry)
 DT
 XX Human CDMF-3, SEQ ID NO:88.
 DE
 XX TGF-beta superfamily; transforming growth factor-beta;
 KW developmental regulation; finger 2 subdomain; basic region;
 KW protein refolding; stability; solubility; osteogenic protein; OP;
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
 KW connective tissue; cartilage; vulnery.

OS Homo sapiens.
 XX
 XX MO200020607-A2.
 PN
 XX 13-APR-2000.
 PD
 XX 07-OCT-1999; 99WO-US023371.
 PF
 XX 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374958.
 XX
 XX (STYC) STRYKER CORP.
 PA
 XX
 XX Oppermann H, Tai M, McCartney J;
 PI
 XX WPI; 2000-303787/26.
 DR
 XX
 XX Transforming growth factor-beta superfamily member mutant induces tissue
 PT morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental
 PT tissue and connective tissue and comprises a substitution in a region of
 PT the finger 2 domain.
 PS
 XX Disclosure; Page 162; 162pp; English.

CC The invention relates to mutant TGF-beta (transforming growth factor-
 CC beta) superfamily members. These mutants comprise one or more amino acid
 CC substitutions in the base region of the finger 2 subdomain, and a C-
 CC terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger
 CC 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an
 CC amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g.,
 CC Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-
 CC beta superfamily proteins regulate developmental processes and include
 CC proteins such as the osteogenic proteins (OPs), bone morphogenetic
 CC proteins (BMPs), growth/differentiation factors (GDFs) and inhibins.
 CC Specific examples of TGF-beta superfamily mutants encompassed by the
 CC invention are the finger 2 subdomain mutants of human osteogenic protein-
 CC 1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for
 CC inducing tissue morphogenesis in bone, non-mineralized skeletal tissue,
 CC dental tissue, connective tissue, brain, liver and nerve tissue. The
 CC proteins can be used in conjunction with a biocompatible matrix e.g.,
 CC collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone,
 CC cartilage and/or other mineralized skeletal or connective tissues e.g.,
 CC ligament, tendon, muscle, fibrocartilage, joint capsule and

CC intervertebral discs. The OP-1 mutants can be used to repair diseased or
 CC damaged mammalian tissue and to prevent or substantially inhibit
 CC immune/inflammatory response-mediated tissue damage and scar tissue
 CC formation following an injury. Compared to the wild-type TGF-beta
 CC superfamily members, the mutant proteins have improved in vitro refolding
 CC properties in a pH range of 6-9, increased solubility in aqueous solution
 CC and improved stability and/or activity. Sequences AAB09519-B09542 and
 CC AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily
 CC proteins referred to in the specification

XX
 XX Sequence 102 AA;
 SQ

Query Match 42.9%; Score 69; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.6e-57;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 CDFPLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDANNVYKQYED 152
 34 CDFPLRSHLEPTNNAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDANNVYKQYED 93

Db 153 MVEVACCCR 161
 94 MVEVACCCR 102

Qy 153 MVEVACCCR 161
 94 MVEVACCCR 102

Db 94 MVEVACCCR 102

RESULT 15
 AAB02824
 ID AAB02824 standard; protein, 102 AA.

AC AAB02824;
 XX
 XX 22-AUG-2000 (first entry)
 DT
 XX Human CDMF-3 construct amino acid sequence SEQ ID NO:88.
 DE
 XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KW bone morphogenic protein; osteogenic protein; mutant; modified;
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KW tissue repair; regeneration; proliferation; differentiation.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200020591-A2.
 PN
 XX 13-APR-2000.
 PD
 XX 07-OCT-1999; 99WO-US023370.
 PF
 XX 07-OCT-1998; 98US-0103418P.
 PR 16-AUG-1999; 99US-00374936.
 XX
 XX (STYC) STRYKER CORP.
 PA
 XX
 XX Oppermann H, Tai M, McCartney J;
 PI
 XX WPI; 2000-303776/26.
 DR
 XX
 XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing
 PT tissue morphogenesis in e.g. bone, comprises a dimer consisting of one
 PT monomer containing domains from two family members.
 PS
 XX Disclosure; Page 149; 149pp; English.

CC The present invention describes a tumour growth factor beta (TGF-beta)
 CC superfamily chimeric protein (I) derived from at least 2 different
 CC members of the superfamily comprising a dimer with one monomer that
 CC contains a finger 2 domain derived from a first family member and a
 CC finger 1 domain and heel domain, both derived from a second family
 CC member. The monomer further comprises a conserved C-terminal cysteine
 CC skeleton. (I) has osteogenic, proliferative and antiinflammatory
 CC activities. The TGF-beta superfamily chimeric proteins (I) are useful for
 CC inducing tissue morphogenesis (i.e. molecules capable of tissue repair

CC and regeneration and/or inhibiting inflammation) in bone, non-mineralised
CC skeletal tissue, dental tissue, connective tissue, brain, liver and nerve
CC and for inducing the proliferation and differentiation of uncommitted
CC progenitor cells in a tissue-specific manner to support new tissue
CC formation. AA429887 to AA429897 and AAB02748 to AAB02824 represent
CC sequences used in the exemplification of the present invention
XX

SQ Sequence 102 AA;

Query Match 42.9%; Score 69; DB 3; Length 102;

Best Local Similarity 100.0%; Pred. No. 1.6e-57;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 CDPELRSHLEPTNHAIIQTILNSMAPDAPASCCVPARLSPISILYIDAANNVVKQYED 152
|||
DB 34 CDPELRSHLEPTNHAIIQTILNSMAPDAPASCCVPARLSPISILYIDAANNVVKQYED 93
|||

QY 153 MVEACGCR 161
|||

DB 94 MVEACGCR 102
|||

Search completed: July 15, 2005, 15:19:01
Job time : 162 secs

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OM protein - protein search, using bw model

Run on: July 15, 2005, 14:59:25 ; Search time 173 Seconds

(without alignments)
476.559 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 880

Sequence: 1 AGSRKANIGCGRRRRRTALAG.....ANNVYKQEDMVVEACGCR 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	880	100.0	461 1 GDF7 MOUSE	P43029 mus musculus
2	712.5	81.0	294 2 Q9BDW9	Q9BDW9 macaca fasc
3	712.5	81.0	447 1 GDF7 CERAE	Q9BDW8 cercopithec
4	712.5	81.0	453 2 Q75RY1	Q75RY1 homo sapien
5	709.5	80.6	450 1 GFD7 HUMAN	Q754P5 homo sapien
6	574.5	65.3	261 2 Q9W6C0	Q9W6C0 brachydanio
7	568.5	64.6	126 2 Q93573	Q93573 gallus galli
8	557	63.3	452 2 Q6HA10	Q6HA10 rattus norv
9	556	63.2	454 2 Q70UT4	Q70UT4 mus musculu
10	553	62.8	201 2 Q6R158	Q6R158 homo sapien
11	553	62.8	455 1 Q6KFI0	Q6KFI0 homo sapien
12	550	62.5	125 1 GDF6 MOUSE	P43028 mus musculu
13	544	61.8	412 2 Q12938	Q12938 brachydanio
14	540.5	61.4	436 1 GDF6 BOVIN	P55106 bos taurus
15	535	60.8	399 2 Q9W753	Q9W753 xenopus lae
16	526	59.8	413 2 Q9DGN4	Q9DGN4 xenopus lae
17	512	58.2	249 2 Q8BRW9	Q8BRW9 mus musculu
18	512	58.2	495 1 GDF5 MOUSE	P43027 mus musculu
19	512	58.2	500 2 Q9W6G0	Q9W6G0 gallus galli
20	510	58.0	501 1 GDF5 HUMAN	P43026 homo sapien
21	507.5	57.7	494 2 Q6K6G0	Q6K6G0 xenopus lae
22	501	56.9	257 2 Q42303	Q42303 brachydanio
23	462	52.5	324 2 Q9YHW9	Q9YHW9 gallus galli
24	426	48.4	621 1 DECA DROPS	P91699 drosophila
25	395	44.9	478 2 Q6J354	Q6J354 petromyzon
26	394.5	44.8	614 2 P91720	P91720 drosophila
27	391	44.4	277 2 Q9Y8Z2	Q9Y8Z2 lampetra ja
28	386	43.9	588 1 DECA DROME	P07713 drosophila
29	385	43.8	422 2 Q6J356	Q6J356 petromyzon
30	380.5	43.2	370 2 Q869A4	Q869A4 achaearana
31	380	43.2	182 2 Q90Y81	Q90Y81 lampetra ja

32	377.5	42.9	178 2 Q25211	Q25211 junonia coe
33	377	42.8	588 2 Q6AMM1	Q6AMM1 drosophila
34	376	42.7	588 2 Q9VOC6	Q9VOC6 drosophila
35	376	42.7	593 1 DECA DROSI	P91706 drosophila
36	375	42.6	411 2 Q9U4T8	Q9U4T8 brachydanio
37	374.5	42.6	361 2 Q96504	Q96504 brachydanio
38	368	41.8	405 2 Q9U5E8	Q9U5E8 psychodera
39	364	41.4	379 2 Q6PUC6	Q6PUC6 anopheles g
40	364	41.4	459 2 Q70307	Q70307 anopheles g
41	363	41.2	289 2 Q9XV08	Q9XV08 strongyloc
42	363	41.2	509 2 Q8W539	Q8W539 archaeter t
43	362	41.1	67 2 Q02784	Q02784 bos taurus
44	362	41.1	399 1 EMB8A MOUSE	P34821 mus musculu
45	361.5	41.1	204 2 Q9X269	Q9X269 tripneustes

ALIGNMENTS

```

RESULT 1
GDF7_MOUSE STANDARD. PRT: 461 AA.
ID GDF7_MOUSE
AC P43029; Q7TMX4; Q99WY1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=Gdf7; Synonyms=Gdf-7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=BALB/c; TISSUE=Testis;
RA Guo J.H., Yu L.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-441 FROM N.A. (ISOFORM 1).
RC STRAIN=TT2;
RX MEDLINE=21136583; PubMed=11238730;
RA Watabe A., Fujita H., Hayashi M., Yamamori T.;
RL "Growth/differentiation factor 7 is preferentially expressed in the
primary motor area of the monkey neocortex.";
J. Neurochem. 76:1455-1464(2001).
RN [3]
RP SEQUENCE OF 311-461 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
Lee S.-J.;
RL "Limb alterations in brachypodism mice due to mutations in a new
member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
RN [4]
RP SUBMIT: Homodimer; disulfide-linked (By similarity).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=P43029-1; Sequence=Displayed;
Name=2;
IsoId=P43029-2; Sequence=VSP_010764;
-1- SIMILARITY: Belongs to the tgf-beta family.
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EMBL; AF525752; AAP97721.1; -
EMBL; AF254571; AAK30843.1; -

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DR EMBL; AF254570; AAK30843.1; JOINED.
DR EMBL; U08339; AAI18780.1; -.
DR PIR; S43296; S43296.
DR HSSP; P12643; 3BMP.
DR MGD; MGI:95690; Gdf7.
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR002400; GF_cyknoc.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta.1.
DR Pfam; PF00688; TGFb_propeptide.1.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Alternative splicing; Cytokine; Glycoprotein; Growth factor; Signal.
KW SIGNAL.
FT SIGNAL.
FT PROPEP.
FT CHAIN.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT DOMAIN.
FT DOMAIN.
FT CARBOHYD.
FT VASPLIC.
SQ SEQUENCE 461 AA; 47890 MW; 92C2511C8EDE478 CRC64;

Query Match
Best Local Similarity 100.0%; Score 880; DB 1; Length 461;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRC 60
DB 301 AGSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRC 360
QY 61 SRKSLHVDFKELGMDWIIAPLDYEAHYCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 120
DB 361 SRKSLHVDFKELGMDWIIAPLDYEAHYCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 420
QY 121 APASCCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161
DB 421 APASCCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 461

RESULT 2
Q9BDW9 PRELIMINARY; PRT; 294 AA.
AC Q9BDW9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OC NCB1_TaxID=9541;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebral cortex motor area;
RA MEDLINE=21136583; PubMed=11238730;
RA Wataabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001)
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF254567; AAK27794.1; -.
DR HSSP; P12643; 3BMP.
DR GO; GO:0008083; F:growth factor activity; IEA.

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DR InterPro; IPR002400; GF_cyknoc.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta.1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON TER.
SQ SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27A39F CRC64;

Query Match
Best Local Similarity 81.0%; Score 712.5; DB 2; Length 294;
Matches 136; Conservative 1; Mismatches 6; Indels 17; Gaps 1;

QY 2 GSRKANIGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRC 61
DB 152 GSPRAVTAGRRRRRTALAGTGAAGSGGGGGGGGGGGGGGGGAGRGHGRGRSRC 194
QY 62 RKSILHVDFKELGMDWIIAPLDYEAHYCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 121
DB 195 RKSILHVDFKELGMDWIIAPLDYEAHYCEGVCDFPLRSHLEPTNHAIQTLLNSMAPDA 254
QY 122 PASCVCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 161
DB 255 PASCVCVPARLSPISILYIDAANNVVKQYEDMVVEACGCR 294

RESULT 3
GDF7_CERAE STANDARD; PRT; 447 AA.
ID GDF7_CERAE;
AC Q9BDW8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Growth/differentiation factor 7 precursor (GDF-7).
GN Name=GDF7;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OC NCB1_TaxID=9534;
[1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RX MEDLINE=21136583; PubMed=11238730;
RX Wataabe A., Fujita H., Hayashi M., Yamamori T.;
RT "Growth/differentiation factor 7 is preferentially expressed in the
RT primary motor area of the monkey neocortex.";
RL J. Neurochem. 76:1455-1464(2001).
CC -1- FUNCTION: May play an active role in the motor area of the primate
CC neocortex.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in the primary area of brain
CC neocortex.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF254569; AAK30842.1; -.
DR EMBL; AF254568; AAK30842.1; JOINED.
DR HSSP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF_beta.1.
DR Pfam; PF00688; TGFb_propeptide.1.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.

```

DR PROSITE, PS00250; TGF_BETA_1; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 318 Potential.
 FT CHAIN 319 447 Growth/differentiation factor 7.
 FT DISULFID 346 412 By similarity.
 FT DISULFID 375 444 By similarity.
 FT DISULFID 379 446 By similarity.
 FT DISULFID 411 411 Interchain (By similarity).
 FT CARBOHYD 80 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 447 AA; 4686 MM; DP46DS91925A8391 CRC64;
 Query Match 81.0%; Score 712.5; DB 1; Length 447;
 Best Local Similarity 85.0%; Pred. No. 4.1e-45;
 Matches 136; Conservative 1; Mismatches 6; Indels 17; Gaps 1;
 QY 2 GSRANLGGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRGRSRCS 61
 DB 305 GSPRAVYAGRRRRRTALAGTGAQGS-----GGGAGRGHGRGRSRCS 347
 QY 62 KSLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 121
 DB 348 KRLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 407
 QY 122 PASCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 408 PASCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 447
 RESULT 4
 ID Q75RY1 PRELIMINARY; PRT; 453 AA.
 AC Q75RY1
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Growth differentiation factor 7.
 GN Name=gdf7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suzuki M., Shimokawa H., Kasugai S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 DR EMBL; AB158468; BABD7014.1; -.
 DR HSSP; P01137; IKLA.
 DR GO; GO:0008083; P:growth factor activity; IEA.
 DR GO; GO:0040007; P:growth; IEA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00019; TGF_beta.1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Growth factor.
 SQ SEQUENCE 453 AA; 47121 MM; 9FD8CB759C63DFID CRC64;
 Query Match 81.0%; Score 712.5; DB 2; Length 453;
 Best Local Similarity 84.9%; Pred. No. 4.2e-45;
 Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1;
 QY 3 SRKANLGGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRGRSRCS 62
 DB 312 SPRAVIGRRRRRTALAGTGAQGS-----GGGAGRGHGRGRSRCS 354
 QY 63 KSLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 122
 DB 355 KRLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 414

QY 123 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 415 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 453
 RESULT 5
 ID GFD7 HUMAN STANDARD; PRT; 450 AA.
 AC G724P5;
 DT 25-OCT-2004 (Rel. 45, Created).
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth/differentiation factor 7 precursor (GDF-7).
 GN Name=GDF7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Guo J.H., Yu L.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May play an active role in the motor area of the primate neocortex (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; AF523269; AAP97720.1; -.
 DR Genew; HGNC:4222; GDF7.
 DR MIM; 604651; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta.1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 19 Potential.
 FT PROPEP 20 321 Potential.
 FT CHAIN 322 450 Growth/differentiation factor 7.
 FT DISULFID 349 415 By similarity.
 FT DISULFID 378 447 By similarity.
 FT DISULFID 382 449 By similarity.
 FT DISULFID 414 414 Interchain (By similarity).
 FT CARBOHYD 83 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 450 AA; 46966 MM; CDB4C617685037BD CRC64;
 Query Match 80.6%; Score 709.5; DB 1; Length 450;
 Best Local Similarity 84.3%; Pred. No. 6.9e-45;
 Matches 134; Conservative 4; Mismatches 4; Indels 17; Gaps 1;
 QY 3 SRKANLGGRRRRRTALAGTGAQGGGGGGGGGGGGGGGAGRGHGRGRSRCS 62
 DB 309 SPRAVIGRRRRRTALAGTGAQGS-----GGGAGRGHGRGRSRCS 351
 QY 63 KSLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 122
 DB 352 KRLHVDPEKLGMDWMIAPLDYEAHCEGVCDFPLRSHLEPTNNAIIQTLLNSMAPDAP 411
 QY 123 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 161
 DB 412 ASCCVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 450

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RESULT 6
O9MECO PRELIMINARY; PRT; 261 AA.
ID O9MECO;
AC O9MECO;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Growth/differentiation factor 7 (Fragment).
GN Name=gdf7;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
X 11
SEQUENCE FROM N.A.
RX MEDLINE=99148135; PubMed=10022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beler D.R., van Doren C.,
RA Poernaler D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily."
RL Genome Res. 9:121-129 (1999).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR HSSP; P08476; INYU.
DR ZFIN; ZDB-GENE-990714-1; gdf7.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR002400; F:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFB.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON TER 1
SQ SEQUENCE 261 AA; 29414 MM; 77346E977036A104 CRC64;

Query Match 65.3%; Score 574.5; DB 2; Length 261;
Best Local Similarity 70.9%; Pred. No. 4.3e-35;
Matches 107; Conservative 10; Mismatches 15; Indels 19; Gaps 1;

QY 11 RRRRTTLAGTRGAGSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSRLHYDFK 70
DB 130 RRRRTTLAGRPGVGPITSGKGG-----RRTRCGRKRLHNVFK 170
QY 71 ELGWDWIITAPLDYEAYHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130
DB 171 ELGWDWIITAPLDYEAYHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDPESTPSCVPSK 230
QY 131 LSPISILYIDANNVVKQYEDMVVEACGR 161
DB 231 LSPISILYIDSGNNVVVKQYEDMVVEACGR 261

RESULT 7
O93573 PRELIMINARY; PRT; 126 AA.
ID O93573;
AC O93573;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative growth/differentiation factor 6/7 (Fragment).
GN Name=gdf6/7;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=99026113; PubMed=9808626;
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
RT of a discrete class of commissural interneurons in the mouse spinal
RT cord."
RL Genes Dev. 12:3394-3407 (1998).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AF089086; AAC97113.1; -.
DR HSSP; P08476; INYU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002400; GF_cysknct.
DR InterPro; IPR002405; Inhibin_alpha.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GFCYSNOT.
DR PRODOM; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor.
FT NON TER 1
SQ SEQUENCE 126 AA; 14265 MM; CB824D280F44A394 CRC64;

Query Match 64.6%; Score 568.5; DB 2; Length 126;
Best Local Similarity 67.5%; Pred. No. 6.3e-35;
Matches 102; Conservative 13; Mismatches 11; Indels 25; Gaps 1;

QY 11 RRRRTTLAGTRGAGSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSRLHYDFK 70
DB 1 RRRRTTLAGRSG-----GGHGRKGRKTRCSRLHNVFK 35
QY 71 ELGWDWIITAPLDYEAYHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDAAPASCVPAR 130
DB 36 ELGWDWIITAPLDYEAYHCGVCDPPLRSHLEPTNHAIIQTLLNSMAPDPESTPSCVPSK 95
QY 131 LSPISILYIDANNVVKQYEDMVVEACGR 161
DB 96 LSPISILYIDSGNNVVVKQYEDMVVEACGR 126

RESULT 8
O6HA10 PRELIMINARY; PRT; 452 AA.
ID O6HA10;
AC O6HA10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth/differentiation factor 16.
GN Name=gdf16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
X 11
SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Brain;
RL Submitted (TAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537426; CAD60936.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cysknct.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFB.
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Db      76 GRRRRRTAFASRH-----GRHGKSRRLRCSKPLHVN 109
Qy      70 KELGMDWIIAPLDYEAYHCGVCDPFLRSHLEPTNNAIIOTLNSMAPDAAPASCCVPA 129
Db      110 KELGMDWIIAPLDYEAYHCGVCDPFLRSHLEPTNNAIIOTLNSMDPGSTPPSCCVPT 169
Qy      130 RLSPISILYIDANNVYKQYEDMVVEACGR 161
Db      170 KLTPTISILYIDAGNNVYKQYEDMVVESCGCR 201

RESULT 11
ID 06KF10 PRELIMINARY; PRT; 455 AA.
AC 06KF10;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Growth differentiation factor 16.
GN Name=GDF16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hind brain;
RA Guo J.H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
DR EMBL; AJ537424; CAD60934.1; -.
DR HSSP; P01137; IALA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0040007; P:growth; IEA.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor.
SQ SEQUENCE 455 AA; 50661 MW; F9F365B99E8C659C CRC64;

Query Match 62.8%; Score 553; DB 2; Length 455;
Best Local Similarity 66.4%; Pred. No. 2.7e-33;
Matches 101; Conservative 11; Mismatches 14; Indels 26; Gaps 1;

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=94195427; Pubmed=8145850; DOI=10.1038/368639a0;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingeley D.M.,
RT Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta superfamily."
RL Nature 368:639-643(1994).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U08338; AAA18779.1; -.
DR PIR; S43295; S43295.
DR HSSP; P08476; INYU.
DR MGD; MGI:95689; Gdf6.
DR InterPro; IPR002400; GF_cyknct.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00438; GF_CYS_KNOT.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Cytokine; Glycoprotein; Growth factor.
FT NON TER 1
FT PROPEP 1
FT CHAIN 5
FT DISULFID 6
FT DISULFID 24
FT DISULFID 53
FT DISULFID 57
FT DISULFID 89
SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B748DA32 CRC64;

Query Match 62.5%; Score 550; DB 1; Length 125;
Best Local Similarity 66.9%; Pred. No. 1.5e-33;
Matches 101; Conservative 10; Mismatches 14; Indels 26; Gaps 1;

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OX NCI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C, Hemmati-Brivanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: Belong to the TGF-beta family.
DR EMBL, AF155125; AAD38402.1; -.
DR HSSP, P08476; INTU.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.
DR GO: GO:0040007; P:growth; IEA.
DR InterPro: IPR002400; GF_cyknoc.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR Pfam: PF00019; TGF_beta_1.
DR PRINTS: PR00438; GFCTSKNOT.
DR PRINTS: PR00669; INHIBINA.
DR Prodom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_beta_1; 1.
KM Growth factor.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B508B517 CRC64;

```

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OM protein - protein search, using sw model

Run on: July 15, 2005, 15:02:31 ; Search time 38 Seconds
(without alignments)
407.655 Million cell updates/sec

Title: US-10-758-210-6

Perfect score: 880

Sequence: 1 AGSRKANIGRRRRRTALAG.....ANNVYKQYEDMVVEACGCR 161

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	830	94.3	151	2	S43296 bone morphogenetic
2	550	62.5	125	2	S43295 bone morphogenetic
3	540.5	61.4	436	2	B55452 cartilage-derived
4	512	58.2	495	2	S43294 bone morphogenetic
5	510	58.0	501	2	JC2347 growth/differentia
6	508.5	57.8	501	2	A55452 cartilage-derived
7	386	43.9	588	2	A26158 decapentaplegic pr
8	353.5	40.2	405	2	I50608 bone morphogenetic
9	351.5	39.9	401	2	JH0689 bone morphogenetic
10	351.5	39.9	408	1	BMH04 bone morphogenetic
11	351	39.9	402	2	A45056 osteogenic protein
12	351	39.9	408	2	S38343 bone morphogenetic
13	351	39.9	420	2	I19541 bone morphogenetic
14	350.5	39.8	400	2	A49147 bone morphogenetic
15	350.5	39.8	408	2	S58791 bone morphogenetic
16	346.5	39.4	393	2	S37073 bone morphogenetic
17	346.5	39.4	394	2	S45355 bone morphogenetic
18	346.5	39.4	396	1	BMH02 bone morphogenetic
19	346.5	39.4	398	2	JH0688 bone morphogenetic
20	346.5	39.4	398	2	JH0687 bone morphogenetic
21	342.5	38.9	353	2	I50607 bone morphogenetic
22	341	38.8	408	2	JH0801 bone morphogenetic
23	341	38.8	430	2	J01184 osteogenic protein
24	341	38.8	461	2	S52408 SPYR1 protein-8
25	338	38.4	510	2	A54798 Vg-1-related prote
26	337	38.3	313	2	I51284 bone morphogenetic
27	337	38.3	431	1	BMH07 bone morphogenetic
28	337	38.3	452	2	I49542 bone morphogenetic
29	336	38.2	454	1	BMH05 bone morphogenetic

30	329	37.4	207	2	S37618 vgr protein - rat
31	327.5	37.2	365	2	T43286 cet-1 protein - Ca
32	327	37.2	513	1	BMH06 bone morphogenetic
33	325	36.9	426	2	JH0690 bone morphogenetic
34	319	36.2	427	2	A40735 TGF beta homolog d
35	307.5	34.9	372	2	C39364 GDF-1 embryonic gr
36	307	34.9	360	2	A29619 Vg1 embryonic grow
37	304	34.5	455	2	A43918 TGF-beta-related p
38	286.5	32.6	472	1	BMH03 bone morphogenetic
39	285	32.4	354	2	S29718 gene nodal protein
40	284.5	32.3	360	2	I53032 bone morphogenetic
41	275.5	31.3	357	2	A29364 GDF-1 embryonic gr
42	275.5	31.3	476	2	JC4646 bone morphogenetic
43	271.5	30.9	478	2	JC4838 bone morphogenetic
44	270.5	30.7	365	2	A46607 growth/differentia
45	265.5	30.2	366	2	A45402 transforming growt

ALIGNMENTS

RESULT 1

S43296 bone morphogenetic protein-related protein (GDF7) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S43296

R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.

A>Title: Limb alterations in brachypodium mice due to mutations in a new member of the

A:Reference number: S43294; MUID:94195427; PMID:8145850

A:Accession: S43296

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-151 <STO>

A:Cross-references: UNIPROT:P43029; GB:U08339; NID:9488465; PIDN:AAA18780.1; PID:948846

C:Superfamily: inhibin

Query Match 94.3%; Score 830; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 2.3e-61;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	11	RRRRRTLAGRGAQSGGGGGGGGGGGGGGGGAGRGGRGRGRGRKSLHYDFK 70
Db	1	RRRRRTLAGRGAQSGGGGGGGGGGGGGGGGAGRGGRGRGRGRKSLHYDFK 60
Qy	71	ELGWDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIIOTLNSMAPDAAPASCVPAR 130
Db	61	ELGWDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIIOTLNSMAPDAAPASCVPAR 120
Qy	131	LSPIISILYIDANNVYTKQYEDMVVEACGCR 161
Db	121	LSPIISILYIDANNVYTKQYEDMVVEACGCR 151

RESULT 2
S43295
bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N:Alternate names: growth and differentiation factor 6
C:Species: Mus musculus (house mouse)
C>Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
A>Title: Limb alterations in brachypodium mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427; PMID:8145850
A:Accession: S43295
A:Molecule type: DNA
A:Residues: 1-125 <STO>
A:Cross-references: UNIPROT:P43028; EMBL:U08338; NID:9488463; PIDN:AAA18779.1; PID:948846
C:Genetics:
A:Gene: Gdf6
C:Superfamily: inhibin

A:Gene: GDB:BMP4; BMP2B
A:Cross-references: GDB:125205; OMIM:112262
A:Map position: 14q22-14q23
C:Superfamily: inhibin
C:Keywords: bone; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-292/Domain: propeptide #status predicted <PRO>
F:293-408/Product: bone morphogenetic protein 4 #status predicted <MAT>
F:143,208,350,365/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 39.9%; Score 351.5; DB 1; Length 408;
Best Local Similarity 49.3%; Pred. No. 1.2e-21;
Matches 66; Conservative 20; Mismatches 29; Indels 19; Gaps 3;

QY 46 GGAGRGH-----GSRKSLHVPFKEIGMDWIIAPLDYEAY 87
DB 276 GHGGRGHTLRRRAKSPKHNQSRKKNCRHSLYVDFSGVGNNDIIVAPRGYQAF 335
QY 88 HCEGVCDPRLSHLEPTNHAIIQTLNSMAPDAAPASCVPARLSPISIIYIDANNVY 147
DB 336 YCHGDCPFPLADHNSNTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVL 394
QY 148 QYEDMVVEACGCR 161
DB 395 NYQEMVVEGCGCR 408

RESULT 11
A45056
osteogenic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 8; OP-2
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45056
R:Ozekaynak, E.; Schlegelberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.
J. Biol. Chem. 267, 25220-25227, 1992
A:Title: Osteogenic protein-2. A new member of the transforming growth factor-beta super
A:Reference number: A45056; MUID:93094231; PMID:1460021
A:Accession: A45056
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-402 <OK>
A:Cross-references: UNIPROT:P34820; GB:M97016; NID:g189389; PIDN:AB01360.1; PID:g189390
A:Experimental source: hippocampus
A:Note: sequence extracted from NCBI backbone (NCBI:P.120189)
C:Genetics:
A:Gene: GDB:BMP8; OP-2
A:Cross-references: GDB:136392
C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 402;
Best Local Similarity 53.2%; Pred. No. 1.2e-21;
Matches 58; Conservative 22; Mismatches 29; Indels 0; Gaps 0;

QY 52 HGRGRSRSRKSILHVPFKEIGMDWIIAPLDYEAYHCEGVCDPRLSHLEPTNHAIIQ 111
DB 293 HGSNGRQVCRHHELYVDFQDGMWIIAPRGYSAIYCEGSCFPLDSQMNATHALQS 352
QY 112 LNSMAPDAAPASCVPARLSPISIIYIDANNVYQYEDMVVEACGC 160
DB 353 LVHLMKNAVPAKCAAPTKLSATSVLYDSSNNVILKRHRMVKACGC 401

RESULT 12
S38343
bone morphogenetic protein 4 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S38343; S33173
R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1174, 289-292, 1993
A:Title: Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal rat calvar
A:Reference number: S38343; MUID:93385158; PMID:8373807

A:Accession: S38343
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-408 <CH>
A:Cross-references: UNIPROT:Q06826; EMBL:Z22607; NID:g296855; PIDN:CAA0329.1; PID:g296
C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 408;
Best Local Similarity 48.1%; Pred. No. 1.2e-21;
Matches 64; Conservative 19; Mismatches 32; Indels 18; Gaps 2;

QY 46 GGAGRGH-----GRRGRSRSRKSILHVPFKEIGMDWIIAPLDYEAYH 88
DB 277 GHGGRGHTLRRRAKSPKHNQSRKKNCRHSLYVDFSGVGNNDIIVAPRGYQAF 336
QY 89 CEGVCDPRLSHLEPTNHAIIQTLNSMAPDAAPASCVPARLSPISIIYIDANNVYK 148
DB 337 CHGDCPFPLADHNSNTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVLK 395
QY 149 QYEDMVVEACGCR 161
DB 396 NYQEMVVEGCGCR 408

RESULT 13
I49541
bone morphogenetic protein 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49541; S29523; B34201
R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mun
J. Biol. Chem. 270, 28364-28373, 1995
A:Title: The mouse bone morphogenetic protein-4 (BMP4) gene: Analysis of promoter utlitz.
A:Reference number: I49541; MUID:96081880; PMID:7499338
A:Accession: I49541
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-420 <RBS>
A:Cross-references: UNIPROT:P21275; GB:L47480; NID:g994733; PIDN:AAC37698.1; PID:g99473
R:Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
Submitted to the EMBL Data Library, December 1990
A:Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) cD
A:Reference number: S29523
A:Accession: S29523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 13-420 <DIC>
A:Cross-references: EMBL:X56848; NID:g50180; PIDN:CAA40179.1; PID:g50181
R:Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, D.
peland, N.G.; Jenkins, N.A.
Genomics 6, 505-520, 1990
A:Title: Chromosomal localization of seven members of the murine TGF-beta superfamily s
A:Reference number: A34201; MUID:90228966; PMID:1970330
A:Accession: B34201
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A:Molecule type: mRNA
A:Residues: 253-420 <DI2>
C:Genetics:
A:Gene: BMP-4
A:Introns: 11/1; 13/7/1
C:Superfamily: inhibin

Query Match 39.9%; Score 351; DB 2; Length 420;
Best Local Similarity 48.1%; Pred. No. 1.2e-21;
Matches 64; Conservative 19; Mismatches 32; Indels 18; Gaps 2;

QY 46 GGAGRGH-----GRRGRSRSRKSILHVPFKEIGMDWIIAPLDYEAYH 88
DB 289 GHGGRGHTLRRRAKSPKHNQSRKKNCRHSLYVDFSGVGNNDIIVAPRGYQAFY 348
QY 89 CEGVCDPRLSHLEPTNHAIIQTLNSMAPDAAPASCVPARLSPISIIYIDANNVYK 148
DB 349 CHGDCPFPLADHNSNTNHAIVQTLVNSV-SSIFPKACVPTLSAISMLYIDEDYKVLK 407

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QY 61 SRKSLHVDPEKELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDA 120
| | | | |
DB 61 SRKSLHVDPEKELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDA 120
| | | | |
QY 121 APASCCVPARLSPISIIYIDANNVVKQYEDMVVEACGCR 161
| | | | |
DB 121 APASCCVPARLSPISIIYIDANNVVKQYEDMVVEACGCR 161
| | | | |

RESULT 2

US-09-945-182-30
; Sequence 30, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; Rosen, Vicki A.
; Woltman, Neil
; Thomson, Gerald H.
; Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/945.182
; FILING DATE: 31-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,324
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-945-182-30

Query Match 98.0%; Score 862; DB 9; Length 240;

Best Local Similarity 97.5%; Pred. No. 1.2e-52;

Matches 157; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGSRKAMAGRRRRRTALAGTGAQSGGSGGGGGGGGGGGAGRGHGRGRSRC 60
| | | | |
DB 80 AGSRKAMAGRRRRRTALAGTGAQSGGSGGGGGGGGGGGAGRGHGRGRSRC 139
| | | | |
QY 61 SRKSLHVDPEKELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDA 120
| | | | |
DB 140 GRKSLHVDPEKELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDA 199
| | | | |
QY 121 APASCCVPARLSPISIIYIDANNVVKQYEDMVVEACGCR 161
| | | | |
DB 200 APASCCVPARLSPISIIYIDANNVVKQYEDMVVEACGCR 240
| | | | |

RESULT 3

US-10-164-279-61
; Sequence 61, Application US/10164279
; Publication No. US20030185792A1
; GENERAL INFORMATION:
; APPLICANT: Keck, P.
; TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
; FILE REFERENCE: CIBT-P04-566
; CURRENT APPLICATION NUMBER: US/10/164,279
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/791946
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 61
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-164-279-61

Query Match 94.3%; Score 830; DB 14; Length 151;

Best Local Similarity 100.0%; Pred. No. 1.5e-50;

Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRRRTALAGTGAQSGGSGGGGGGGGGGGAGRGHGRGRSRSKSLHVDPK 70
| | | | |
DB 1 RRRRTALAGTGAQSGGSGGGGGGGGGGGAGRGHGRGRSRSKSLHVDPK 60
| | | | |
QY 71 ELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDAAPASCCVPAR 130
| | | | |
DB 61 ELGDDWIIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIOTLLNSMAPDAAPASCCVPAR 120
| | | | |
QY 131 LSPISIIYIDANNVVKQYEDMVVEACGCR 161
| | | | |
DB 121 LSPISIIYIDANNVVKQYEDMVVEACGCR 151
| | | | |

RESULT 4

US-09-945-182-2
; Sequence 2, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; Rosen, Vicki A.
; Woltman, Neil
; Thomson, Gerald H.
; Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/945.182
; FILING DATE: 31-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,324
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618

```

1      REFERENCE/DOCKET NUMBER: 5202-D
2      TELECOMMUNICATION INFORMATION:
3      TELEPHONE: 617 498-8260
4      TELEFAX: 617 876-5851
5      INFORMATION FOR SEQ ID NO: 2:
6      SEQUENCE CHARACTERISTICS:
7          LENGTH: 294 amino acids
8          TYPE: amino acid
9          TOPOLOGY: linear
10     MOLECULE TYPE: protein
11     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
12     US-09-945-182-2
13
14     Query Match      81.0%; Score 712.5; DB 9; Length 294;
15     Bect Local Similarity 84.9%; Pred. No. 3,7e-42;
16     Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1
17
18     QY      3 SRKANLGGRRRRRTLAGTGAQSGGGGGGGGGGGGGGGGAGRGHGRGRSRCSR 62
19     DB      153 SPRAVIGRRRRRTLAGTGRQSG-----GGAGRGHGRGRSRCSR 195
20
21     QY      63 KSLHVFKELEGNDWMIAPLDYEAHCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAP 122
22     DB      196 KPLHVFPELEGNDWMIAPLDYEAHCEGLCGFPLRSHLEPTNHAIIQTLLNSMAPDAAP 255
23
24     QY      123 ASCCVPARLSPISILYIDANNVYKQYEDMYEACGCR 161
25     DB      256 ASCCVPARLSPISILYIDANNVYKQYEDMYEACGCR 294
26
27 RESULT 5
28 US-09-945-182-34
29 Sequence 34, Application US/09945182
30 Patent No. US20020160494A1
31 GENERAL INFORMATION:
32 APPLICANT: Celeste, Anthony J.
33     Wozney, John
34     Rosen, Vicki A.
35     Wolfman, Neil
36     Thomsen, Gerald H.
37     Melton, Douglas A.
38     TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
39     NUMBER OF SEQUENCES: 35
40     CORRESPONDENCE ADDRESS:
41     ADDRESSEE: GENETICS INSTITUTE, INC.
42     STREET: 87 CambridgePark Drive
43     CITY: Cambridge
44     STATE: Massachusetts
45     COUNTRY: USA
46     ZIP: 02140
47     COMPUTER READABLE FORM:
48     MEDIUM TYPE: floppy disk
49     OPERATING SYSTEM: IBM PC compatible
50     SOFTWARE: PatentIn Releasee #1.0, Version #1.25
51     CURRENT APPLICATION DATA:
52     APPLICATION NUMBER: US/09/945,182
53     FILING DATE: 31-Aug-2001
54     CLASSIFICATION: <Unknown>
55     PRIOR APPLICATION DATA:
56     APPLICATION NUMBER: 08/808,124
57     FILING DATE: <Unknown>
58     ATTORNEY/AGENT INFORMATION:
59     NAME: Lazar, Steven R.
60     REGISTRATION NUMBER: 32,618
61     REFERENCE/DOCKET NUMBER: 5202-D
62     TELECOMMUNICATION INFORMATION:
63     TELEPHONE: 617 498-8260
64     TELEFAX: 617 876-5851
65     INFORMATION FOR SEQ ID NO: 34:
66     SEQUENCE CHARACTERISTICS:
67     LENGTH: 388 amino acids
68     TYPE: amino acid

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; MOLECULE TYPE: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-945-182-34

Query Match      81.0%; Score 712.5; DB 9; Length 388;
Best Local Similarity 84.9%; Pred. No. 4,6e-42;
Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1,

OY 3 SRKANLGGRRRRRTALAGTGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSR 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 247 SPRAVIGGRRRRRTALAGTRTAQGS-----CGGAGRGHGRGRSRCSR 289

OY 63 KSLHVDPEKLGMDWIIAPLDYEAYHCEGVCDFPLNSHLEPTNHAIIQTLLNSMAPDAAP 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 290 KPLHVDPEKLGMDWIIAPLDYEAYHCEGVCDFPLNSHLEPTNHAIIQTLLNSMAPDAAP 349

OY 123 ASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 ASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 388

RESULT 6
US-10-366-345-43
; Sequence 43, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-345-43

Query Match      81.0%; Score 712.5; DB 15; Length 388;
Best Local Similarity 84.9%; Pred. No. 4,6e-42;
Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1;

OY 3 SRKANLGGRRRRRTALAGTGAQSGGGGGGGGGGGGGGGGGAGRGHGRGRSRCSR 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 247 SPRAVIGGRRRRRTALAGTRTAQGS-----CGGAGRGHGRGRSRCSR 289

OY 63 KSLHVDPEKLGMDWIIAPLDYEAYHCEGVCDFPLNSHLEPTNHAIIQTLLNSMAPDAAP 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 290 KPLHVDPEKLGMDWIIAPLDYEAYHCEGVCDFPLNSHLEPTNHAIIQTLLNSMAPDAAP 349

OY 123 ASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 ASCCVPARLSPISILYIDANNVVKQYEDMVVEACGCR 388

RESULT 7
US-10-188-246-12
; Sequence 12, Application US/10188246
; Publication No. US20030087274A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W..
; APPLICANT: Boldog, Ferenc.
; APPLICANT: Caeman, Stacie.
; APPLICANT: Edinger, Shlomit.
; APPLICANT: Gerlach, Valerie.
; APPLICANT: Gorman, Linda.
; APPLICANT: Li, Li.
; APPLICANT: Malysankar, Uriel.
; APPLICANT: Paturajan, Meera.
; APPLICANT: Peyman, John.

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: PRIOR FILING DATE: 2002-07-03
: PRIOR APPLICATION NUMBER: US 60/303,500
: PRIOR FILING DATE: 2001-07-05
: PRIOR APPLICATION NUMBER: US 60/305,403
: PRIOR FILING DATE: 2001-07-13
: PRIOR APPLICATION NUMBER: US 60/307,011
: PRIOR FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 60/308,187
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: US 60/309,416
: PRIOR FILING DATE: 2001-08-01
: PRIOR APPLICATION NUMBER: US 60/311,740
: PRIOR FILING DATE: 2001-08-09
: PRIOR APPLICATION NUMBER: US 60/343,553
: PRIOR FILING DATE: 2001-12-21
: NUMBER OF SEQ ID NOS: 62
: SOFTWARE: PERL Program
: SEQ ID NO 18
: LENGTH: 450
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 748635ICD1
US-10-481-698-18

Query Match      81.0%; Score 712.5; DB 16; Length 450;
Best Local Similarity 84.9%; Prd. No. 5,2e-42;
Matches 135; Conservative 3; Mismatches 4; Indels 17; Gaps 1;

3 SRKANIIGRRRRRTTALAGTRGAQGGGGGGGGGGGGGGAGRGHGRGRSFCSR 62

```

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Db      309   SPRAVIGRRRRRTALAGTAAQS-----GGGAGRGHGRGRSRCSR    351

Qy      63     KSLANDPKELGWMDWIIAPLDYEAHYCEGVCFPLSHLEPTTHAIIQTLLNSMAPDAP    122
              |||||::|||||
Db      352   KPRLHVFKEKGWDWIIAPLDYAYHCEGLCDFPLSHLEPTTHAIIQTLLNSMAPDAP    411

Qy      123   ASCCVPARLSPISILYTDANNVVYQYEDMVEACGCR    161
              |||||
Db      412   ASCCVPARLSPISILYTDANNVVYQYEDMVEACGCR    450

RESULT 9
US-09-945-182-28
; Sequence 28, Application US/09945182
Patent No. US20020160949A1
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